Prediction of Regulatory Networks for Non-Model Organisms

Rachita Sharma, Patricia Evans, Virendra Bhavsar

A regulatory network of an organism is represented by a set of genes and their regulatory relationships, which indicate how genes affect production of other gene products. We are developing a system to predict the regulatory relationships of a non-model organism, about which less information is known, using information about the regulatory relationships of a more thoroughly investigated model organism. The genes that act as regulatory elements are identified for the non-model organism using the available regulatory element information of the model organism. The initial phase of this system has been developed for identification of regulatory elements and has been tested on two pairs of organisms, by mapping the regulatory elements from Yeast to *Arabidopsis thaliana* and from Yeast to *Escherichia coli*. The results indicate higher mapping in the first pair as Yeast and *Arabidopsis thaliana* belong to the same group, eukaryotes (which contain DNA in nucleus of the cell), and so tend to have more similarity in regulatory relationships, while *Escherichia coli* is from another group, prokaryotes (which lack a distinct nucleus in the cell). Next, the patterns in regulatory relationships from the regulatory networks will be recognized and mapped from the model organism to the non-model organism. The mapped regulatory relationships of the non-model organism will then be confirmed using relevant available data.